

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/549,317  
Source: 1FWO  
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IFWO

## RAW SEQUENCE LISTING

DATE: 06/30/2006

PATENT APPLICATION: US/10/549,317

TIME: 10:10:34

Input Set : A:\81356247.APP

Output Set: N:\CRF4\06302006\J549317.raw

3 <110> APPLICANT: SOEJIMA, KENJI  
 4 NAKAGAKI, TOMOHIRO  
 5 MATSUMOTO, MASANORI  
 6 FUJIMURA, YOSHIHIRO  
 8 <120> TITLE OF INVENTION: CONSTRUCT COMPRISING REGION RECOGNIZED BY ANTIBODY  
 9 AGAINST VON WILLEBRAND FACTOR-SPECIFIC CLEAVING  
 10 PROTEASE  
 12 <130> FILE REFERENCE: 81356/247  
 14 <140> CURRENT APPLICATION NUMBER: 10/549,317  
 15 <141> CURRENT FILING DATE: 2005-09-16  
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP04/003602  
 18 <151> PRIOR FILING DATE: 2004-03-17  
 20 <150> PRIOR APPLICATION NUMBER: JP 2003/71979  
 21 <151> PRIOR FILING DATE: 2003-03-17  
 23 <160> NUMBER OF SEQ ID NOS: 21  
 25 <170> SOFTWARE: PatentIn Ver. 3.3  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 1427  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: Homo sapiens  
 32 <400> SEQUENCE: 1  
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 34 1 5 10 15  
 36 Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His  
 37 20 25 30  
 39 Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser  
 40 35 40 45  
 42 Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly  
 43 50 55 60  
 45 Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu  
 46 65 70 75 80  
 48 His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His  
 49 85 90 95  
 51 Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala  
 52 100 105 110  
 54 Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu  
 55 115 120 125  
 57 Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr  
 58 130 135 140  
 60 Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr  
 61 145 150 155 160  
 63 Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu  
 64 165 170 175

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66 Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
67      180      185      190
69 Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
70      195      200      205
72 Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
73      210      215      220
75 Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
76 225      230      235      240
78 Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
79      245      250      255
81 Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
82      260      265      270
84 Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
85      275      280      285
87 Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
88      290      295      300
90 Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
91 305      310      315      320
93 Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
94      325      330      335
96 Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
97      340      345      350
99 Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
100      355      360      365
102 Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
103      370      375      380
105 Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
106 385      390      395      400
108 Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
109      405      410      415
111 Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
112      420      425      430
114 Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
115      435      440      445
117 Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
118      450      455      460
120 Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
121 465      470      475      480
123 Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
124      485      490      495
126 Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
127      500      505      510
129 Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
130      515      520      525
132 Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
133      530      535      540
135 Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
136 545      550      555      560
138 Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val

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139          565          570          575
141 Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
142          580          585          590
144 Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
145          595          600          605
147 Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
148          610          615          620
150 Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
151 625          630          635          640
153 Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
154          645          650          655
156 Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
157          660          665          670
159 Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
160          675          680          685
162 Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
163          690          695          700
165 Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
166 705          710          715          720
168 Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
169          725          730          735
171 Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
172          740          745          750
174 Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
175          755          760          765
177 Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
178          770          775          780
180 Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
181 785          790          795          800
183 Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
184          805          810          815
186 Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
187          820          825          830
189 Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
190          835          840          845
192 Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
193          850          855          860
195 Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
196 865          870          875          880
198 Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
199          885          890          895
201 Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
202          900          905          910
204 Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
205          915          920          925
207 Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
208          930          935          940
210 Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
211 945          950          955          960

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213 Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
214          965          970          975
216 Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
217          980          985          990
219 Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys Ser
220          995          1000          1005
222 Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser Leu Gly Pro Cys
223      1010          1015          1020
225 Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg Ser Val Ala Cys Val
226 1025          1030          1035          1040
228 Gln Leu Asp Gln Gly Gln Asp Val Glu Val Asp Glu Ala Ala Cys Ala
229          1045          1050          1055
231 Ala Leu Val Arg Pro Glu Ala Ser Val Pro Cys Leu Ile Ala Asp Cys
232          1060          1065          1070
234 Thr Tyr Arg Trp His Val Gly Thr Trp Met Glu Cys Ser Val Ser Cys
235          1075          1080          1085
237 Gly Asp Gly Ile Gln Arg Arg Arg Asp Thr Cys Leu Gly Pro Gln Ala
238 1090          1095          1100
240 Gln Ala Pro Val Pro Ala Asp Phe Cys Gln His Leu Pro Lys Pro Val
241 1105          1110          1115          1120
243 Thr Val Arg Gly Cys Trp Ala Gly Pro Cys Val Gly Gln Gly Thr Pro
244          1125          1130          1135
246 Ser Leu Val Pro His Glu Glu Ala Ala Ala Pro Gly Arg Thr Thr Ala
247          1140          1145          1150
249 Thr Pro Ala Gly Ala Ser Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu
250          1155          1160          1165
252 Phe Ser Pro Ala Pro Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu
253 1170          1175          1180
255 Asn Ser Val Gln Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr
256 1185          1190          1195          1200
258 Gly Thr Ile Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala
259          1205          1210          1215
261 Ile Gly Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser
262          1220          1225          1230
264 Ser Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu
265          1235          1240          1245
267 Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser Ser
268 1250          1255          1260
270 Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys Gly Arg Pro Gly Gly
271 1265          1270          1275          1280
273 Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu Ala Pro Glu Thr Phe Tyr
274          1285          1290          1295
276 Arg Glu Cys Asp Met Gln Leu Phe Gly Pro Trp Gly Glu Ile Val Ser
277          1300          1305          1310
279 Pro Ser Leu Ser Pro Ala Thr Ser Asn Ala Gly Gly Cys Arg Leu Phe
280          1315          1320          1325
282 Ile Asn Val Ala Pro His Ala Arg Ile Ala Ile His Ala Leu Ala Thr
283 1330          1335          1340
285 Asn Met Gly Ala Gly Thr Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile

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286 1345          1350          1355          1360
288 Arg Asp Thr His Ser Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val
289          1365          1370          1375
291 Leu Tyr Trp Glu Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu
292          1380          1385          1390
294 Gly Phe Leu Lys Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu
295          1395          1400          1405
297 Gln Ser Trp Val Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys
298          1410          1415          1420
300 Glu Gly Thr
301 1425
304 <210> SEQ ID NO: 2
305 <211> LENGTH: 30
306 <212> TYPE: DNA
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 2
310 ctggagcacg acggcgcgcc cggcagcggc          30
313 <210> SEQ ID NO: 3
314 <211> LENGTH: 30
315 <212> TYPE: DNA
316 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 3
319 atgtgcaaca ctcaggcctg cgagaagacc          30
322 <210> SEQ ID NO: 4
323 <211> LENGTH: 30
324 <212> TYPE: DNA
325 <213> ORGANISM: Homo sapiens
327 <400> SEQUENCE: 4
328 ccaacctgac cagtgtctac attgcccaacc          30
331 <210> SEQ ID NO: 5
332 <211> LENGTH: 21
333 <212> TYPE: DNA
334 <213> ORGANISM: Homo sapiens
336 <400> SEQUENCE: 5
337 ctggagccct gccacctag g          21
340 <210> SEQ ID NO: 6
341 <211> LENGTH: 62
342 <212> TYPE: DNA
343 <213> ORGANISM: Homo sapiens
345 <400> SEQUENCE: 6
346 tccgtcgact cttatcactt atcgtcacg tccttgtagt cgtcccacac gcagcgcgcc 60
347 cg          62
350 <210> SEQ ID NO: 7
351 <211> LENGTH: 62
352 <212> TYPE: DNA
353 <213> ORGANISM: Homo sapiens
355 <400> SEQUENCE: 7
356 tccgtcgact cttatcactt atcgtcacg tccttgtagt cgcgccatg cactgctgct 60
357 at          62

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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; Xaa Pos. 3,4,6,7,9,10

**VERIFICATION SUMMARY**

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Input Set : A:\81356247.APP

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L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0